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It is well known that only a small fraction of extant microbial life has been identified. Metagenomics, the direct sequencing and characterization of genes and genomes present in complex microbial ecosystems (e.g., metagenomes), has revolutionized the practice of microbiology by bypassing the hurdle of pure culture isolation. Metagenomics shows promise of advancing our understanding of the diversity, function, and evolution of the uncultivated majority.

Metagenomics as a field arose in the 1990s after the application of molecular biology techniques to genomic material directly extracted from microbial assemblages present in diverse habitats, including the human body. The application of metagenomic approaches allows for the acquisition of genetic/genomic information from the viruses, bacteria, archaea, fungi, and protists forming complex assemblages. The field of metagenomics addresses the fundamental questions of which microbes are present and what their genes are potentially doing.

In the mid-2000s, the availability of high-throughput or next-generation sequencing technologies propelled the field by lowering the monetary and time constraints imposed by traditional DNA sequencing technologies. These advances have allowed the scientific community to examine the microbiome of diverse environments/habitats, follow spatial and temporal changes in community structure, and study the response of the communities to treatment or environmental modifications.

In 2012, the publication of the large-scale characterization of the microbiome of healthy adults created high expectations about the influence of the microbiota in human health and disease. With the publication of the results of the Human Microbiome Project, metagenomics has emerged as a major research area in microbiology, particularly, when it comes to the characterization of the role of microbiota in complex disorders, such as obesity.

With contributions by leading researchers in the field, we provide a series of chapters describing best practices for the collection and analysis of metagenomic data, as well as the promises and challenges of the field. The chapters have been dedicated to different aspects of metagenomics. Chapter 1 provides an end-to-end overview of the metagenomic pipeline and its challenges. Chapter 2 showcases SMRT, one of the third-generation sequencing platforms, and its use in metagenomics. As high abundance of ribosomal RNA (rRNA) transcripts is a major hurtle for the application of transcriptomics to microbial communities, Chapter 3 describes methodology that can reduce the "noise" rRNA imposes on this type of studies. Chapters 4 and 5 showcase some of the computational approaches that are used to analyze the whole-community metagenome sequence data and available software, and highlight future research directions. The statistical challenges and solutions for cross-sectional and longitudinal data sets are explored in Chapters 6 and 7, respectively. Chapter 8 presents a historical perspective of the microbiome studies, the societal impact of microbial communities, and the challenges ahead for metagenomics, while advances in virome studies are explored in Chapter 9. A perspective on the current efforts, challenges, and the future of metagenomic is presented in Chapter 10.

This book is intended for researchers, teachers, students, and the citizen scientists contemplating performing microbial metagenomics

studies. For microbiologists generating metagenomic next-generation sequencing data, the book will provide an introduction and support to the computational and statistical specifics of the data. For the statisticians and computational scientist contemplating working with metagenomic data, it will provide some of the initial background needed. For the community, in general, it will provide the basis for further investigation of this transformative and fascinating field.

We would like to thank all authors for their contributions. We need to acknowledge the public and private funding entities that made this technological and conceptual advance a possibility, as well as the researchers and consortia that broke the grounds for those innovations to flourish. Last, we would like to thank Elsevier for the short book format and allowing a more focused and didactic approach.